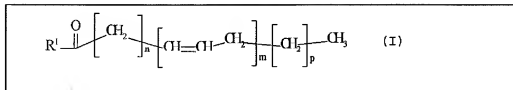


AMENDMENTS TO THE CLAIMS

Listing of Claims

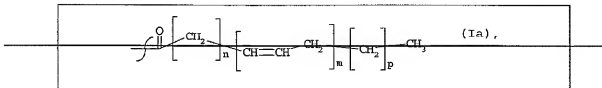
1. (Currently Amended) A process for the production of compounds in transgenic plants, wherein said compounds are comprised of general Formula I:



wherein $R^1 = -\text{OH}$, coenzyme A (thioester), phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid or a radical of general Formula II:



wherein $R^2 = \text{H}$, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, phosphatidylserine, phosphatidylinositol, sphingolipid, glycosphingolipid, glycosphingolipid or saturated or unsaturated C_2-C_{24} alkylcarbonyl-; and $R^3 = \text{H}$, saturated or unsaturated C_2-C_{24} alkylcarbonyl-; and wherein R^2 and R^3 independently of one another represent a radical of general Formula Ia:



wherein $n = 3, 4$ or 6 ; $m = 3, 4$ or 5 ; and $p = 0$ or 3 , and said compounds comprise at least 1% by weight of the total fatty acid content of said transgenic plants, which process comprises the following steps:

introducing, into a plant:

at least one first nucleic acid sequence which encodes a polypeptide with an $\Delta 6$ -desaturase activity;

at least one second nucleic acid sequence which encodes a polypeptide with a $\Delta 6$ -elongase activity; and,

optionally, a third nucleic acid sequence which encodes a polypeptide with a $\Delta 5$ -desaturase activity; and

growing and harvesting the transgenic plant.

2-3. (Canceled).

4. (Currently amended) The process of claim 1, wherein R^2 and R^3 independently of one another are unsaturated C_{16} , C_{18} , C_{20} or C_{22} -alkylcarbonyl- with one, two, three, four or five double bonds.

5. (Previously presented) The process of claim 1, wherein the plant is an oil crop.

6. (Previously presented) The process of claim 1, wherein the plant is selected from the group consisting of soya, peanut, oilseed rape, canola, linseed, evening primrose, verbascum, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.

7. (Previously presented) The process of claim 1, wherein the compounds of general Formula I are obtained from the transgenic plants by pressing or extraction, and said compounds are in the form of oils, fats, lipids or free fatty acids.

8. (Previously presented) The process of claim 7, wherein the oils, fats, lipids or free fatty acids are refined.

9. (Previously presented) The process of claim 1, wherein saturated or unsaturated fatty acids present in the compounds are liberated.

10. (Previously presented) The process of claim 9, wherein the saturated or unsaturated fatty acids are liberated by alkaline hydrolysis or enzymatic cleavage.

11. (Previously presented) The process of claim 1, wherein the compounds comprise at least 5% by weight, of the total fatty acid content of the transgenic plants.

12. (Currently amended) The process of claim 1, wherein the nucleic acid sequence that encodes the polypeptide with $\Delta 6$ -desaturase activity, $\Delta 6$ -elongase activity or $\Delta 5$ -desaturase activity is comprises a nucleic acid sequence selected from the group consisting of:

- a) a nucleic acid sequence that contains the sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31,
- b) ~~a nucleic acid sequences encoding a polypeptide comprising the which, owing to the degeneracy of the genetic code, are obtained by back-translation of an~~ amino acid sequence ~~contains the sequence~~ of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32, and
- c) ~~derivatives of a nucleic acid sequence that contains the sequence of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29 or SEQ ID NO: 31 which encode encoding a derivative polypeptide that contains having at least 90% homology with the amino acid sequence of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32, and which has at least 50% homology at the amino acid level, wherein enzymatic activity of the~~

~~derivative polypeptide is not substantially reduced as compared to said polypeptide-~~
has essentially the same enzymatic activity.

13. (Previously presented) The process of claim 1, wherein one or more of the first, second, and optionally third nucleic acid sequences are linked with one or more regulatory signals in a nucleic acid construct.

14. (Previously presented) The process of claim 13, wherein the nucleic acid construct comprises additional biosynthetic genes of fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyl transferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxigenases, triacylglycerol lipases, allene oxide synthases, hydroperoxide lyases fatty acid elongase(s) and combinations thereof.

15. (Previously presented) The process of claim 1, wherein the first, second and optionally third nucleic acid sequences are stably integrated in the plant.

16. (Previously presented) The process of claim 1, wherein the plant is selected from the group consisting of plant cells, plant tissues, plant organs, plant leaves, plant roots, plant stems, intact plants, plant tubers, plant seeds, and cellular parts of any of the preceding.

17. (Previously presented) The process of claim 7, wherein the pressing or the extraction is performed without supplying heat.

18. (Currently amended) The process of claim 12, wherein two or more of the first, second and third nucleic acid sequences are selected from said the group of nucleic acid sequences as set forth in claim 12.

19. (Currently amended) The process of claim 12, wherein the first, second and third nucleic acid sequences are selected from said the group of nucleic acid sequences as set forth in claim 12.

20. (Currently amended) The process of claim 13, wherein the first, second and third nucleic acid sequences are linked to with one or more regulatory signals in said nucleic acid construct.
21. (New) The process of claim 1, wherein the plant is a dicot.
22. (New) The process of claim 1, wherein the plant is tobacco or linseed.